Gencole Version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

January 16, 2003 (10.42)]7 , Smarch time 9 21429 Seconds Pun on:

(without alignments) 58.517 Million cell updates/sec

US-09-856-070-25 Title: Perfect score:

1 MI.RI.Q 5 Sednence: Scoring table:

BLOSUM62 Gapop 10 0 , Gapext 0.5

283224 scqs, 96131422 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Ma+ch 09 Maximum Match 100%

Database :

PIR_73:*

pirl:* pir2:* pir3:* pir4:* Pred $N_{\rm c}$ is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMAPIES

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esult		Ouery				
No.	Score	Match	Length	a i	Ĺ.	Description
		100.0	120	C4	P72450	hypothetical prote
C3			157	C4	1169461	
٣	23	100 n	160	2	A71300	
4		100.0	196	_	911454	
2	23	100.0	196	C4	A36554	
9	<u>د</u> ع	100 0		C+	A48992	
7	m Ci	100.0		C)	AF1561	Ω.
Œ.	e. Ci	100	077	e i	AG1204	ABC trassporter, A
6	m Ci	100.0	244	C 4	836703	qene 8 protein - e
10	۳. تع	100.0	245	-	WZBEA7	gene 8 protein . c
11	23	100.0	C	C1	AB1553	B. subtilis YibH p
12	er Ci	100.0		CI	A11195	π,
13	۳ د	100.0		~ 1	T41101	lin dependent
14	e e e	100 0		٠.	AP2737	aspartute carbamay
15		100.0	322	C I	H82583	aspartate carbamoy
16	£3	100.0	322	C 1	AP3593	aspartate carbamoy
17		100.0		C 1	236335	U2 SERNP 40K prote
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20			334	C4	A56144	aspartate carbamoy
21		100.0	334	C I	1183555	aspartate carbame,
Ci		100.0	355	C 4	F96020	probable from ARC
53		100.0	364	C4	897518	(AY007523) aspaila
24			055	C+	356560	7
S. C.		00	400	C.	P91241	
93			338	: 1	586132	
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38			453	C a	142428	mitochoudrial proc
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23	100.0	457	7	T50402	probable mitochond
2.3	100.0	505	7	164189	amidophosphoribosv
2	100.0	505	C 4	AD0338	amidophosphoribosy
<u>ر.</u> دا	100	ς Ω 1	C.	145889	egrin - boyine
53	100.0	586	-1	A34400	ezrin [validated]
53	100.0	586	۰.	B41129	carin - monse
53	100.0	610	C4	T19333	hypothetical prote
<u>بر.</u>	0.00:	630	C 4	147177	hypothetical prote
53	100.0	748	7	T49633	glucan 1,4-alpha-a
7.	0.001	785	C1	1185036	hypothetical prote
æ.	100 0	404	C4	T00475	probable disease r
53	100.0	1428	Ċŧ	T39475	probable ATP depen
e E	100.0	1690	C1	T13030	microtubule bindin
2	91.3	100	C	A81097	primosoma: replica
7.7	91.3	100	~	C81845	primosomal replica
21	91.3	109	C)	H95038	hypothetical prote

RESULT 1
F72450
F72450
F72450
Sypothers a Protein AFE2250 Aeropyrum pernix (strain Kl)
C)Species: Aeropyrum pernix
C,Nat. 20 Ang 1949 #sequence_rovision 20 Aug-1959 #text_change 09 Jun 2030
C)Accession: F72450

Cymicazaton, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res. 6, 83-101, 1999
A.Title. Complete genome sequence of an aerobic hyper-thermophilic Grenarchaeon, Aero A.Kecference number. A72450; Mulb:1938/39; PMID:1038/2956
A.Recession: F72450

A:Status: preliminary

A; Molecule type: DNA

oldby Alectionsky Nitrogshipsoussy prionichAAMizez is Propositosfyssy Pyryg A mostducs: [120 cKAW.]
A.Cross references. Eddu Aborgond. Nicogslabous; prenchadalla C.Seperimental Source: strain Kl C.Seperimental Source: strain Kl A.Gene: APE2250 C.Superfamily: Aeropyrum pernix hypothetical protein APE2250

0; Gaps Query Match 1995.9%; Score 23; EH 2; Longth 120; Hest Local Similarity 100.0%; Pred. No. 35; Autobas 5; Conservative 0; Mismatches 6; Indels ů, Indels 0, Mismatches

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1 MLRLQ 5

1 1

H69461

Conserved hypothetical protein AF1697 - Archaeoglobus fulgidus C.Species, Archaeoglobus fulgidus C.Sata. CESTAGES 797 #sequent-traising of provided #text_change of cet-1999 C.Aa ession: #69461

E.Klenk, H.P., Clarton, R.A., Tomb, J.F., White, O., Neison, K.E., Ketchum, K.A.) Dod J. Fleischmann, K.D., Quackenbush, J., Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E. Glode, A. Shou, L., Gverhenk, K.; Serayov, J. P., Werdman, J.F.; McDonald, L. Nature 390, 364-370, 1997.
A.Authors, Ctterback, L.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O., Kase, C.E., Venter, J.C.
A.Tiller The complete genome sequence of the hyperthermophilic, sulfate-reducing arch A.Perence number. A65250, MUID-J8642343, PMIL: J863475

A.Status, preliminary, modeled acid sequence not shown, translation not shown

A,Molecule type: DNA A,Recidaes, 1 157 - KLEZ A.Cross-references: GR-AEconomes, GB:AEcon/M2; NIEcq2nds109; PIDN:AAB89557.1; PID:q264 C.Saperfamily, Methancococcas januaschii conserved nypothelical protein MJ1553

Guery Match

100 0%, Scott 23; UB 2, cength 157;

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Caps

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A;Title: Nucleotide sequence of mouse L19 ribosomal protein cDNA isolated in screenin A;Relerence number: A;6554; MUID:91090840; PMID:1702292
A;Accession: A36554
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Cancer Res. 53, 1408, 1408, 1993
Astitle: High-level expression of the ribosomal profein [19 in human breast tumors the
A;Reference number: A48992; MUID:93185086; PMID:8095182
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A.Experimental source: breast cancer (coll line, MCF-7
A.Notic: sequence extracted from NCH backbone (NCHIN:127871, NCHIP:127872)
R.Kumabe, T.; Sohma, Y.; Yamamoto, T.; Nucleic Acids Res. 20, 2598, 1992
A.Tille: Human cDNAs encoding elongation lactor lgamma and the ribosomal protein L19.
A.Reterence number: S22655; MOID: 92282147; FMID:1598220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispate: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change l3-Aug-1999
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C.Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 13-Auq-1999
C.Accession: A48992; S22656
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A;Note: this sequence was submitted to the EMBL Data Library, December 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A)Cross-references: GR:MF2952; NID:4198642; PIDN:AAB48630.1, FID:4198643
C;Superfamily: rat ribosomal protein E19
C;Reywords: protein blosynthesis; ribosome
                                                               A;Cross-references: GB:M30264; NID:q205112; PIDN:AAA41503.1; PID:q554467
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DNA Cell Biol. 9, 697-703, 1990
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                                                                                                                                                                                                                                                                                   100.0%; Score 23; DB 1; Length 196; 100.0%, Pred. No. 58;
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                                                                                                                                                                                                                         C: Keywords: protein biosynthesis; ribosome; RNA binding
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C:Superfamily: rat ribosomal protein 1.19
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Matches 5: Conservative
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Matches 5; Conservative
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      A;Molecule type: DNA
A,Rusidues, 111 145 KRH2>
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rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, I.; McDo
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-160 <COL>
A;Cross references: GB:AE(001239) GE-AE000520; MES-33222937; PIDN-AAG65623 1; PIP-3332294
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A;Reference number: A56846; MILD:95309903; DMID:7789970
A:Accession: A56846
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Proc. Natl. Acad. Sci. U.S.A. B6, 6604-6605, 1989
A.Tille. N. A strategy to dispert and isolate an intron-containing gene in the presence of A.Relerem number: 159154; MHID:87814; PMID:2771953
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A/Cross-references: EMHL:X82202; NID:9732917; PID:9762995
A/Note: the differences in the central region are due to a frameshift truot resulting
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A;Reference number: A71250; MJID:98332770; PMID:9665876
A;Accession: A71300
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                                                                                                                                                                                                                                                                                                      conserved hypotherical protein TP0650 · syphilis spirochete
Cispecies: Troponema pd Hidum subsp. pd Hidum (syphilis spirochete)
Cibate: 24 · ul 1948 #sevyuenee_revision; 24 · D; 1998 #fext_change 28 Js1-2000
CiAccession: A71300
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A;Mesidues: 4-12 «CHA2»
A;Note: The protein is designated as ribosomal protein L19
R;Davies, B.; Protein
Genomics 25, 372, 380, 1995
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100.0%;
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Matches 5; Conservative
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0; Gaps

Fri Jan 17 09:19:15 2003

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A.Status, preliminary, translated from Objemblyobbd.
"Nymblecule type: DNA
A.Residues, 1944 -77EL
A.Residues, 1944 -77EL
A.Residues, EMBLARESTORY, NID:926650; FIDN.ARCSUSS7.1; FID.3200605
A.Experimental source: strain NS80567
                                                                                                                                                                                                                                                             NyAlternate names: B2 protein
C:Species: equine herpesvirus 4
C.Date - 69-Tuni1994 *sequence_forishe: i2 May 1995 *text_change 11:5al 2000
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A.Note: host Equins caballus (domestic horse)
...az. W. 2ept-192 ascquence_revision 30 Scp-1992 atext_change 16-Jul-1999
C.Accession: 136795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AfMolocule type: DNA
A. residues. 1 241 - E.C.
A. residues. 1 241 - E.C.
A. residues. 1 241 - E.C.
A. Gross - Erreteror Comparation of St. Perry, J.; Cullbane, A.A.; Davison, A.J.
E. Fellord, E.A.; Watson, M.S.; Perry, J.; Cullbane, A.A.; Davison, A.J.
J. Gen. Virol. 79, 1197-1203, 1998
A.Title: The DNA sequence of equine herpsyring-4.
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A,Residues: 1.245 <TEL>
A,Ctoss-reterences: GELM86664; NID:q330791; PIDN:AAB02443.1; PID:q330800
A,Ctoss-reterences: GELM86664; NID:q330791; PIDN:AAB02443.1; PID:q330800
R(Tellord, E A P : Watson, M S.; McBride, R.; Davison, A.J.
Virology 189, 304-316, 1992
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 23; DB 2; Length 244; 100.0%; Pred, No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virology 189, 304-316, 1992
A;Title: The DNA sequence of equine herpesvirus-1.
A;Reference number: A41831, MUD:92295566; PMID:1418606
A;Contents: annotation: possible protein-coding trames
A;Note: heither amino acid not nucleotide sequence is given c;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F.Telford, E.A.E., Watson, M.S., McBilde, K., Davison, A.J.,
submitted to GenBank, March 1992
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A.Accession: 136795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Reference number: "122173, Muliu.98264497; PMID:9603335
A, Accession: T42551
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                                                                                                                                                                                                                                                                                                                                                                                                     R:Riggio, P. submitted to the EMBL Data Library, November 1989
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                                                                                                                                                                                                                                     gene 8 protein - equine herpesvirus 4
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nes 5; Conservative
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A;Accession: $36703
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      1 MI.RI.Q 5
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A.Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Malok, C.; Schupeter, T. Simces, N.; Titchen, A.; Vass, H.; Wahland, A. Anticher, Comparative genomics of Listeria species.
A.Reference number: AR107; MTLP:2157279; FMIE:11E79889
A.Recession: AF1561
A.Status: proliminary
A.Residues: 1-220 -GLAS
A.Residues: 1-220 -GLAS
A.CLOSS IELEGEORE GR AL. GOLZ, FIEN TAPGESCI, FIEU-115414456, RSPDEJRGOLZ6
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Anthors Kreft, J., Kohn, M., Konst, F., Kurapkat, G.; Madueno, E.; Mattournam, A.; M. Arthors Kreft, J., Kohn, M., Torrez, A., Vazquez-Beland, J.A.; Voxs, H., Wehland, A.; Efference number: ABIO7; Muthor215x229; PMID:11679669
Astrocketon and Alice and Anthor215x229; PMID:11679669
Astrocketon and Anthor215x229; PMID:11679669
Astrocketon and Anthor215x229; PMID:11679669
Astrocketon and Anthor215x229; PMID:11679669
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C.Species: Listeria monocytogenes
C.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #fext_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABC transporter, ATP-binding protein homolog lin1031 [imported] - Listeria innocua (stra
                                                                                                                                                                                                                                     0
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A:Experimental Source: Strain EGD-e
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A:Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Species. Listeria innocua
C.Date: 27:Nov 200] #smgschot_froision 27:Nov 200] #text_dargo 27 Nov 2001
                                                                                                                                                                                                                                     0; Caps
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Best Local Similarity 100 0%; Pred. No. 66;
                                                                                                                                                                100.0%; Score 23; DH 2; Length 196; 100.0%; Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 23; DB 2; Length 220;
100.0%; Pred. No. 66;
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                                                                                                                                                                                                                              0; Mismatches
A;Cross-references: GDH:128847; OMIM:180466
                                                                                                 C.Keywords: profein biosynthesis: ribosome
                               A:Map position: 17q11-17q11
C:Superfamily: rat ribosomal protein L19
                                                                                                                                                                                               Best Local Similarity 100.0%;
Matches 5; Conservative C
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Best Local Similarity
5; Conserva
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A:Gene: lin1031
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AsMap position: circular chromosome
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Hest Local Similarity 100.0%;
Watches 5; Conservative 0
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Conservative 0
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es 5; Conservé
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A.Molecule type: DNA
A.Pesidues: 1-313 <KUR>
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C; Accession: T41101
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A:Gene: SPDI
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A;Authors: Kreft, J.; Kuhu, M.; Aunst, F.; Authors, E.; Maduene, F., Maiteurnam, A.; Ma ok, C.; Schlueter, T.; Simosa, N.; Tierrez, A.; Vazquez Boland, J.A.; Voss, H.; Wehland, A.T.H. Comparative genomics of Listeria species.
A;Reterence number: AB1077; MUID:21547279; PMID:11679669
                                                                                                                                                                                                                                             Richasch D. Franqeul, L.; Huchricser, C., Amend, A., Baquero, F., Berche, D.; Hibecker J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Lomes, L.M.; Karst. U.
Science 294, 849 822, 2021
A;Authors: Kreft, J.; Knim, M.; Nunst, F.; Kurapkat, G.; Madueno, F.; Maitentnam, A.; Machere, T.; Simose, N.; Herrez, A.; Vargeer-Beland, J.A.; Voss, H.; Wehland, A. P.; M.; Vielerepee number: ARIO77-MIID-21547279; PMID-11673669
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                                                                                                                                                 B. subtilis Yjbli protein homolog lin0963 [imported] - Listeria innocua (strain Clip11262 C) Species: Listeria innocua innocua (Cliate: 27-Nov-2001 #sequence_revision 27 Nov 2001 #text_change 27 Nov-2001 C.Aeression: AH1553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B. subtilis Vjb4 protein homolog ImcOG64 (imported) - Listeria mengegrags (strain EG)
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C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Listeria monocytogenes
C.Date: 27 Nov 2001 *sequence_revision 27 Nov 2001 *text_change 27 Nov 2001
C.Accession: AD1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cispecies: Schizosaccharomyces pombe
Cibate: 03 Dec:1999 #sequence_revision 03-bec-1999 #text_change 31-Tan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Srote 23; NH 2; Longth 272; 100.0%; Pred. No. 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Experimental source: strain Clip11262
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Matches 5: Conserv
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                        44 MURUA 37
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47 MLRLO 41
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                                                                                                 RESULT 11
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assurtate carbamcy; transferase [imported] Agrobacterium tunnefacions (strain 058, D. C.Species. Agrobacterium tunnefacions
C.Species. Agrobacterium tunnefacions
C.Date: 11-Jan-2002 #sequence_revision 11.Jan-2002 #text_change 01 Peb-2002
C.Date: 11-Jan-2002 #sequence_revision 11.Jan-2002 #text_change 01 Peb-2002
C.Date: 12.Date: 12.Da
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A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Keterence number: A85515; MIIID-20345717; PMID-10910347
A;Nute: for a complete list of authors see reference number A59328 below
A,Accession. H82583
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                                                                                                                                                                                                                                                                                                                                                                                                                     A)Residues: 1/288 <PUR>
A)Residues: 1/288 <PUR>
A)Cross references: DMBL:AL031535, PIDN.CAA20750,1, GSPUH:GN00068; SPDE:SPCT1664.11
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A,Experimental source: strain C58 (Dupont)
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C.Date: 18-Ang-2000 #sequenc_revision 20-Aug-2000 #text_change 02 Sep 2000
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R:Purnelle, B.; Gotteau, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMHL Data Library, September 1998
A:Reference number: 221964
A:Recession: 14101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 23; DB 2; Length 288;
100.0%; Pred, No. 87;
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A:Molecule type: DNA
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A:Residues: 1-322 <SIM>
A:Cross-references: Gh-Re004035; GB:AE003R49; NID:g9107371; PIIN:AAP85025.1; GSPDH:GN001
A:Experimental source: strain 9a5c
B:Simpson, A.J.G.: Refnach, E.C.; Arruda, P.; Abreu, E.A.; Acencio, M.; Alvarenqa, R.; A. Simpson, A.J.G.: Refnach, E.C.; Arruda, P.; Abreu, E.A.; Acencio, M.; Alvarenqa, R.; A. Briones, M. R.; Bueno, M. R. P.; Canargo, A. P.; Ferreira, A.J.S.
submitted to Genhank, June 2000
A:Authors: Ferreira, A.C.A.; Ferrey, J. S.; Franca, S.C.; Franco, M.C.; Frohm
J.D. Junqueira, M.L.; Remper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, A.M. B.N.; Madeira, A. M. M. A.; Madeira, M. M. A.; Madeira, A.M. B.N.; Madeira, M. M. A.; Madeira, M. M.; Silva Jr., W.A.; Galiveira, M. A.; Sahasak, M. H.; Vallada, H.; Van Silva, A.A.; Verjovski Almeida, S.; Vettore, A.L.; Z. A.; Reference number: A55328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A)Contents: annotation
C;Genetics:
A;Gene: XF2226
C;Superfamily: ornithine carbamoyitransferase; aspartate/ornithine carbamoyitransferase
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237 MEREQ 241
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Search completed: January 16, 2003, 16:57:53 Job time : 9.21429 secs

